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Citation
Pe'er, I., Shamir, R. Spectrum alignment: efficient resequencing by hybric
Conf Intell Syst Mol Biol 8:260-268, 2000.

Summary
Proc Int Conf Intell Syst Mol Biol 2000;8:260-8

Spectrum alignment: efficient resequencing by hybridization.

Pe'er I, Shamir R.

Department of Computer Science, Tel Aviv University, Israel. izik@math.t

Recent high-density microarray technologies allow, in principle, the detern
mers that appear along a DNA sequence, for k = 8 - 10 in a single experin
standard chip. The k-mer contents, also called the spectrum of the sequer
sufficient to uniquely reconstruct a sequence longer than a few hundred b.
devised a polynomial algorithm that reconstructs the sequence, given the
homologous sequence. This situation occurs, for example, in the identifica
nucleotide polymorphisms (SNPs), and whenever a homologue of the targ
known. The algorithm is robust, can handle errors in the spectrum and ass
knowledge of the k-mer multiplicities. Our simulations show that with reali:
SNPs, the algorithm correctly reconstructs a target sequence of length up
nucleotides when a polymorphic sequence is known. The technique is ger
handle profiles and HMMs as input instead of a single homologous sequer

Electronic Manuscript
None available

Technical Program

ISMB2000

August 19, Saturday

Tutorials - All Day

August 20, Sunday

Networks and Modeling
Moderator: TBA

Keynote
08:30 - 09:15
Gerald Edelman, The Neurosciences Institute
How Matter Becomes Imagination: From Brain Dynamics to Consciousness

09:15 - 09:40
Eugene P. van Someren, Lodewyk F.A. Wessels, Marcel J.T. Reinders, Delft University of Technology
Linear Modeling of Genetic Networks from Experimental Data

09:40 - 10:05
Mathius Fellenberg, Biomax Informatics GmbH
Max-Planck-Institute f. Biochemistry
Kaj Albermann, Alfred Zollner, Biomax Informatics GmbH
H.W. Mewes, Max-Planck-Institute f. Biochemistry
Jean Hani, Biomax Informatics GmbH
Integrative Analysis of Protein Interaction Data

Coffee
10:05 - 10:30

10:30 - 10:55
Maura Cárdenas-García, Jaime Lagúnez-Otero, Instituto de Química, UNAM, Ciudad Universitaria
Nikolai Korneev, Instituto Nacional de Astrofísica Optica y Electrónica
Efficient Attractor Analysis Based on Self-dependent Subsets of Elements--An Application to Signal Transduction Studies

10:55 - 11:20
Yukako Tohsato, Hideo Matsuda, Akihiro Hashimoto, Osaka University
A Multiple Alignment Algorithm for Metabolic Pathway Analysis Using Enzyme Hierarchy

11:20 - 11:45
Michael P.S. Brown, HNC
Small Subunit Ribosomal RNA Modeling Using Stochastic Context-Free Grammars

11:45- 01:30
Lunch, Job Fair Recruitment Event, and BOFs

Networks and Modeling Related to Microarrays
Moderator: TBA

Keynote
01:30 - 02:15
J. Andrew McCammon, Chemistry and Biochemistry, UC San Diego
Dynamics of Molecular Recognition

02:15 - 02:40
Soumya Raychaudhuri, Joshua M. Stuart, Xuemin Liu, Peter M. Small, Russ B. Altman, Stanford
University
Pattern Recognition of Genomic Features with Microarrays: Site Typing of Mycobacterium
Tuberculosis
Strains

02:40 - 03:05
Andrea Califano, Gustavo Stolovitzky, Yuhai Tu, IBM Computational Biology Center
Analysis of Gene Expression Microarrays for Phenotype Classification

Coffee
03:05 - 03:30

03:30 - 03:55
Roded Sharan, Ron Shamir, Tel-Aviv University
CLICK: A Clustering Algorithm with Applications to Gene Expression Analysis

03:55 - 04:20
Yizong Cheng, University of Cincinnati
George M. Church, Harvard Medical School
Biclustering of Expression Data

04:20 - 04:45
Norbert Brändle, Horng-Yang Chen, Horst Bischof, Vienna University of Technology; Hilmar
Lapp
Novartis Research Institute, Vienna
Robust Parametric and Semi-parametric Spot Fitting for Spot Array Images

05:00 - 07:00 Posters, Software Demos, Exhibits
07:00 - 09:00 Industry Night

August 21, Monday

Protein Structure and Modeling I

Moderator: TBA

Keynote
08:30 - 09:15
Harold A. Scheraga, Chemistry and Chemical Biology, Cornell University
Ab Initio Folding of Proteins

09:15 - 09:40
Piero Fariselli, Rita Casadio, University of Bologna
Prediction of the Number of Residue Contacts in Proteins

09:40 - 10:05
Iddo Friedberg, Tommy Kaplan, Hanah Margalit, The Hebrew University-Hadassah Medical School
Glimmers in the Midnight Zone: Characterization of Aligned Identical Residues in Sequence-Dissimilar Proteins Sharing a Common Fold

Coffee
10:05 - 10:30

10:30 - 10:55
Pierre Baldi, Gianluca Pollastri, University of California Irvine; Claus A. F. Andersen, Søren Brunak, The Technical University of Denmark
Matching Protein b-Sheet Partners by Feedforward and Recurrent Neural Networks

10:55 - 11:20
Maxim Shatsky, Zipora Y. Fligelman, Tel Aviv University, Ruth Nussinov, Tel Aviv University, IRSP-SAIC Lab of Experimental and Computational Biology
Haim J. Wolfson, Tel Aviv University
Alignment of Flexible Protein Structures

11:20 - 11:45
Lukasz Jaroszewski, Adam Godzik, The Burnham Institute
Search for a New Description of Protein Topology and Local Structure

11:45 - 12:10
J. Michael Sauder; Roland L. Dunbrack Jr., Fox Chase Cancer Center
Genomic Fold Assignment and Rational Modeling of Proteins of Biological Interest

Lunch and BOFs
12:10 - 01:30

Protein Structure and Modeling II
Moderator: TBA

Keynote
01:30 - 02:15
Leroy Hood, Institute for Systems Biology, University of Washington
Computing Life and Biological Complexity

02:15 - 02:40
Golan Yona, Michael Levitt, Stanford University
Towards a Complete Map of the Protein Space Based on a Unified Sequence and Structure Analysis of All Known Proteins

Gene Regulation I
Moderator: TBA

02:40 - 03:05
Harmen J. Bussemaker, University of Amsterdam
Hao Li, University of California, San Francisco
Eric D. Siggia, Rockefeller University
Regulatory Element Detection Using a Probabilistic Segmentation Model

Coffee
03:05 - 03:30

03:30 - 03:55
Jaak Vilo, Alvis Brazma, European Bioinformatics Institute EBI
Inge Jonassen, University of Bergen
Alan Robinson, European Bioinformatics Institute EBI
Esko Ukkonen, University of Helsinki
Mining for Putative Regulatory Elements in the Yeast Genome using Gene Expression Data

03:55 - 04:20
Steve Hampson, Pierre Baldi, Dennis Kibler, Suzanne B. Sandmeyer, University of California Irvine
Analysis of Yeast's ORF Upstream Regions by Parallel Processing, Microarrays, and Computational Methods

04:20 - 04:45
Ian Holmes, University of California Berkeley
William J. Bruno, Los Alamos National Laboratory
Finding Regulatory Elements Using Joint Likelihoods for Sequence and Expression Profile Data

05:00 - 07:00 Posters, Software Demos, Exhibits

August 22, Tuesday

Back to the Top | August 20 (Sun) | August 21 (Mon) | August 23 (Weds)

Sequence - Alignments, Families and Phylogeny I
Moderator: TBA

Keynote
08:30 - 09:15

Gene Myers, Celera Genomics Corporation, Rockville, MD
A Whole Genome Assembly of Drosophila and a Progress Report on the Human Genome

09:15 - 09:40
Eleazar Eskin, William Noble Grundy, Columbia University
Yoram Singer, Hebrew University
Protein Family Classification using Sparse Markov Transducers

09:40 - 10:05
Itsik Pe'er, Ron Shamir, Tel Aviv University
Spectrum Alignment: Efficient Resequencing by Hybridization

**Coffee
10:05 - 10:30**

10:30 - 10:55
Bogdan Dorohonceanu, C.G. Nevill-Manning, Rutgers University
Accelerating Protein Classification Using Suffix Trees

10:55 - 11:20
Rainer Spang, Duke University; Marc Rehmsmeier, Jens Stoye, German Cancer Research Center
Sequence Database Search Using Jumping Alignments

11:20 - 11:45
Mary E. Cosner, Ohio State University
Robert K. Jansen, University of Texas-Austin
Bernard M.E. Moret, University of New Mexico
Linda A. Raubeson, Central Washington University
Li-San Wang, Tandy Warnow, Stacia Wyman, University of Texas-Austin
A New Fast Heuristic for Computing the Breakpoint Phylogeny and Experimental Phylogenetic Analyses of Real and Synthetic Data

11:45 - 12:10
Dan Gusfield, University of California, Davis
A Practical Algorithm for Optimal Inference of Haplotypes from Diploid Populations

**Lunch, BOFs, and ISCB Business Session (open meeting)
12:10 - 01:50**

Gene Regulation II
Moderator: TBA

01:50 - 02:15
Alexander Zien, Robert Kuffner, Ralf Zimmer, Thomas Lengauer
GMD-German National Research Center for Information Technology
Analysis of Gene Expression Data with Pathway Scores

02:15 - 02:40
Pavel A. Pevzner, Sing-Hoi Sze, University of Southern California
Combinatorial Approaches to Finding Subtle Signals in DNA Sequences

02:40 - 03:05
Saurabh Sinha, Martin Tompa, University of Washington
A Statistical Method for Finding Transcription Factor Binding Sites

Coffee
03:05 - 03:30

03:30 - 03:55
Vineet Bafna, Daniel H. Huson, Celera Genomics Corp.
The Conserved Exon Method for Gene Finding

04:00 - 06:00 Posters, Software Demos, Exhibits

06:00 - 10:00 ISMB 2000 Reception, San Diego Zoo

August 23, Wednesday

Methods
Moderator: TBA

08:30 - 09:15
Keynote: *G. Christian Overton Lecture: Reading the Book of Life*
David B. Searls
SmithKline Beecham Pharmaceuticals

09:15 - 09:40
Hagit Shatkay, Stephen Edwards, W. John Wilbur, Mark Boguski, National Center for
Biotechnology Information
Genes, Themes, and Microarrays Using Information Retrieval for Large-Scale Gene Analysis

09:40 - 10:05
Chris Bailey-Kellogg, John J. Kelley III, Cliff Stein, Bruce Randall Donald, Dartmouth College
Reducing Mass Degeneracy in SAR by MS by Stable Isotopic Labeling

Coffee
10:05 - 10:30

● **10:30 - 10:55**
Vanathi Gopalakrishnan, Bruce G. Buchanan, John M. Rosenberg, University of Pittsburgh
Intelligent Aids for Parallel Experiment Planning and Macromolecular Crystallization

10:55 - 11:20
Denys Proux, Xerox Research Centre Europe
François Rechenmann, INRIA Rhône-Alpes
Laurent Julliard, Xerox Research Centre Europe
A Pragmatic Information Extraction Strategy for gathering Data on Genetic Interactions

11:20 - 11:45
Robert F. Murphy, Michael V. Boland, Meel Velliste, Carnegie Mellon University
Toward a Systematics for Protein Subcellular Location: Quantitative Description of Protein Localization Patterns and Automated Analysis of Fluorescence Microscope Images

11:45 - 12:10
Zhengyan Kan, Washington University
Warren Gish, Washington University School of Medicine
Eric Rouchka, Washington University
Jarret Glasscock, Washington University School of Medicine
David States, Washington University
UTR Reconstruction and Analysis Using Genomically Aligned EST Sequences

● **Lunch and BOFs**
12:10 - 01:30

Sequence - Alignments, Families and Phylogeny, II
Moderator: TBA

Keynote
01:30 - 02:15
Minoru Kanehisa, Institute for Chemical Research, Kyoto University
Graph Comparison and Path Computation Methods for Predicting Molecular Networks from Genome Information

02:15 - 02:40
Robin McEntire, SmithKline Beecham Pharmaceuticals
Peter Karp, SRI-International
Neil Abernethy, InGenuity
David Benton, SmithKline Beecham Pharmaceuticals
Gregg Helt, University of California Berkeley
Matt DeJongh, NetGenics
Robert Kent, Ontologos
Anthony Kosky, GeneLogic
Suzanna Lewis, University of California Berkeley
● Dan Hodnett, NetGenics
Eric Neumann, 3rd Millenium
Frank Olken, Lawrence Berkeley Livermore Laboratory

Dhiraj Pathak, SmithKline Beecham Pharmaceuticals
Luca Toldo, Merck KgaA
Thodoros Topaloglou, GeneLogic
An Evaluation of Ontology Exchange Languages for Bioinformatics

02:40 - 03:05
Mark Craven, David Page, Jude Shavlik, Joseph Bockhorst, Jeremy Glasner, University of Wisconsin
A Probabilistic Learning Approach to Whole-Genome Operon Prediction

Coffee
03:05 - 03:30

03:30 - 03:55
Stefan Kurtz, Enno Ohlebusch, Chris Schleiermacher, University of Bielefeld
Jens Stoye, German Cancer Research Center
Robert Giegerich, University of Bielefeld
Computation and Visualization of Degenerate Repeats in Complete Genomes

03:55 - 04:20
Mathieu Blanchette, Benno Schwikowski, Martin Tompa, University of Washington
An Exact Algorithm to Identify Motifs in Orthologous Sequences from Multiple Species

04:20 - 04:45
Best Poster and Paper Awards Session

ISMB | Agenda | For additional assistance, please consult the Contact Information page.